AMENDMENTS TO THE DRAWINGS

One replacement drawing sheet (FIG. 1) is submitted herewith. Label 19 was added to Figure 1(E) to correspond to the tube, as described in the specification on page 11 at line 6.

Attachment: Replacement Sheet (Fig. 1)

REMARKS

I. Formal Matters

A. Status of Claims

Claims 1-8 are pending. Claims 1-3 are rejected. Claims 4-7 are objected to. New claim 8 is added.

In the present Amendment, each of claims 1-7 is amended to improve clarity by replacing the recitation "DNA or RNA" with "polynucleotide" and the recitation "DNAs or RNAs" with "polynucleotides."

Claim 1 is amended to replace the recitation "a sample" with "the sample," and the recitation "an base sequence" with "the base sequence."

Claim 1 is also amended to replace the recitation "comprising the steps of" with the recitation "consisting essentially of the steps of."

Claim 1 is also amended to include the recitation "at least one kind of probe." Support for this amendment may be found in the present specification at, for example, page 5, lines 5-11.

Claim 2 is amended to improve clarity by replacing the recitation "any of the sample . . . and the probe . . . is not immobilized" with "none of the sample . . . or the probe is immobilized"

Claim 3 is amended to add the recitation "to detect plural base sequences of interest." Support for this amendment may be found, for example, in the present specification at page 5, lines 5-11.

Claim 4 and claim 5 are both amended to depend from "claims 1 or 2," instead of claims 1 to 3 and 1 to 4, respectively.

Claim 5 is amended to improve clarity by replacing the recitation "hybridization with a complimentary chain DNA thereof" with "hybridization with a polynucleotide chain complementary thereto."

Claim 6 is amended to improve clarity by replacing the recitation "wherein the complementary chain DNA or RNAs" with "wherein the polynucleotide chains complimentary to the probe polynucleotides."

Claim 7 is amended to improve clarity by replacing the recitation "wherein the immobilized complementary chain DNA or RNAs" with "wherein the immobilized polynucleotide chain complimentary to the probe polynucleotides."

No new matter has been added, and entry of the Amendments to the Claims is respectfully requested.

B. Claim to Priority

The Examiner acknowledged a claim to priority. However, the present application is a non-convention application with no claim to priority.

C. Amendments to the Specification

The present specification at page 14, lines 19-20, incorrectly refers to seven (7) DNA sequences in the sequence listing. The sequence listing only discloses six (6) sequences. The Amendment corrects the typographical error.

In addition, the present specification at page 5, lines 8-9, is corrected to read ". . . even when the amount of sample DNA or RNA is little . . ." to correct a typographical error. The present specification at page 6, lines 14-15, for example, supports this disclosure.

D. Amendments to the Drawings

According to the present specification at page 11, Figure 1(E) should have a tube 19. The tube in Fig. 1(E), however, is missing label 19. A replacement drawing sheet is provided with the Amendment.

II. Detailed Action

A. Objection to the Claims

Claims 4-7 are objected to under 37 C.F.R. § 1.75(c) as allegedly being in improper form because a multiple dependent claim cannot depend on a multiple dependent claim.

As noted above, each of claims 4 and 5 is amended to depend from claims 1 or 2. Accordingly, none of the present multiple dependent claims (i.e., claims 3-5 and 8) depends on a multiple dependent claim.

B. Claim Rejections - 35 U.S.C. § 102

Claims 1-3 are rejected under 35 U.S.C. § 102(b) as allegedly being anticipated by the article Nucleic Acids Research 22 (22) : 4840-4841 (1994) by Somers et al. ("Somers").

Applicants submit that this rejection should be withdrawn because Somers does not disclose or render obvious the method for the detection of a base sequence of interest recited by the present claims.

Somers discloses the use of the Exonuclease-Amplification Capture Coupled Technique ("EXACCT"). In EXACCT, PCR products are incubated with exonuclease to produce two single-strand DNAs of approximately half the length of the original DNA. Then, the single-strand PCR product is hybridized to two different detection probes; a biotinylated capture probe and a digoxigenin labeled probe. Next, the product is transferred to a streptavidan-coated

microtiter plate and incubated with T4 DNA ligase. When there is perfect complementarity in the Point-EXACCT method, the T4 DNA ligase covalently joins the 5' biotinylated probe and the 3' detection probe. The joined probes can be detected by anti-digoxigenin antibody.

In view of the above, the Examiner asserts that Somers appears to disclose a method similar to claim 1 of the present invention.

However, the presently claimed subject matter is distinguishable from Somers.

For example, Somers and the EXACCT method both require that at least two probes hybridize with a sample DNA or RNA to detect one sequence (or point mutation) of interest. Further, Somers requires the use of T4 DNA ligase for detection. In contrast, the present invention can identify a sequence of interest with only one probe.

In addition, the method disclosed by the present invention can be implemented with *multiple* probes to detect *multiple*, non-contiguous base sequences of interest. Accordingly, the present claims recite a method whereby each probe can detect a sequence present anywhere along the chain or on separate chains.

In contrast, Somers and the EXACCT method do not disclose, or fairly suggest, a method whereby more than one non-contiguous base sequence may be detected in a single assay. More significantly, the base sequences detected by the two Somers probes must be contiguous.

Applicants amended claim 1 by replacing the recitation "comprising the steps of" with the recitation "consisting essentially of the steps of." The "consisting essentially of" language excludes any step that affects the essential characteristics of the invention. For example,

"consisting essentially of" language excludes the T4 DNA ligase step required for detection in the Point-EXACCT method.

Applicants also kindly direct the Examiner's attention to claim 8. Claim 8 is patentable for additional independent reasons.

Claim 8 recites the method of claims 1 or 2 wherein "plural kinds of probe polynucleotides are used to detect plural, non-contiguous base sequences of interest."

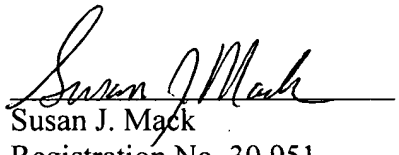
As noted above, Somers teaches a method of detection whereby two probes are required for the detection of one contiguous base sequence. Thus, incorporating the recitation "non-contiguous" emphasizes a distinction between the present invention and the Point-EXACCT method.

III. Conclusion

In view of the above, reconsideration and allowance of this application are now believed to be in order, and such actions are hereby solicited. If any points remain in issue which the Examiner feels may be best resolved through a personal or telephone interview, the Examiner is kindly requested to contact the undersigned at the telephone number listed below.

The USPTO is directed and authorized to charge all required fees, except for the Issue Fee and the Publication Fee, to Deposit Account No. 19-4880. Please also credit any overpayments to said Deposit Account.

Respectfully submitted,



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